

1	60
a) NDVARGIVKA DVAQNNGLY GQGQVAVAD TGLDTGRNDS SMHEAFRGKI TALYALGRTN	
b) NDVARGIVKA DVAQNNGLY GQGQLVAVAD TGLDTGRNDS SMHEAFRGKI TALYALGRTN	
c) NDVARGIVKA DVAQNNFGLY GQGQIVAVAD TGLDTGRNDS SMHEAFRGKI TALYALGRTN	
61	120
a) NANDPNGHGT HVAGSVLGNA LNKGMAPQAN LVFQSIMDSS GGLGGLPSNL NTLFSQAWNA	
b) NASDPNGHGT HVAGSVLGNA LNKGMAPQAN LVFQSIMDSS GGLGGLPSNL NTLFSQAWNA	
c) NANDPNGHGT HVAGSVLGNA TNKGMAPQAN LVFQSIMDSG GGLGGLPANL QTLFSQAYSA	
121	180
a) GARIHTNSWG APVNGAYTAN SRQVDEYVRN NDMTVLFAAG NEGPNSGTIS APGTAKNAIT	
b) GARIHTNSWG APVNGAYTAN SRQVDEYVRN NDMTVLFAAG NEGPNSGTIS APGTAKNAIT	
c) GARIHTNSWG APVNGAYTTD SRNVDDYVRK NDMTILFAAG NEGPGSGTIS APGTAKNAIT	
181	240
a) VGATENYRPS FGSLADNP NH IAQFSSRGAT RDGRIKPDVT APGTFILSAR SSLAPDSSFW	
b) VGATENYRPS FGSADNP NH IAQFSSRGAT RDGRIKPDVT APGTFILSAR SSLAPDSSFW	
c) VGATENLRPS FGSYADNP NH VAQFSSRGPT RDGRIKPDVM APGTYILSAR SSLAPDSSFW	
241	300
a) ANYNSKYAYM GGTSMATPIV AGNVAQLREH FIKNRGITPK PSLIKAALIA GATDVGLGYP	
b) ANYNSKYAYM GGTSMATPIV AGNVAQLREH FIKNRGITPK PSLIKAALIA GATDVGLGYP	
c) ANHDSKYAYM GGTSMATPIV AGNVAQLREH FVKNRGVTPK PSLIKAALIA GAADVGLGFP	
301	360
a) SGDQGWGRVT LDKSLNVAYV NEATALATGQ KATYSFQAQA GKPLKISLVW TDAPGSTTAS	
b) SGDQGWGRVT LDKSLNVAYV NEATALATGQ KATYSFQAQA GKPLKISLVW TDAPGSTTAS	
c) NGNQGWGRVT LDKSLNVAFV NETSPLSTSQ KATYSFTAQA GKPLKISLVW SDAPGSTTAS	
361	420
a) YTLVNDLDLV ITAPNGQKYV GNDFSYPYDN NWDGRNNVEN VFINAPQSGT YTIEVQAYNV	
b) YTLVNDLDLV ITAPNGQKYV GNDFSYPYDN NWDGRNNVEN VFINAPQSGT YIEVQAYNV	
c) LTLVNDLDLV ITAPNGTKYV GNDFTPYDN NWDGRNNVEN VFINAPQSGT YTVEVQAYNV	
421	433
a) PSGPQRFSLA IVH	
b) PSGPQRFSLA IVH	
c) PVSPQTFSLA IVH	

Fig. 1

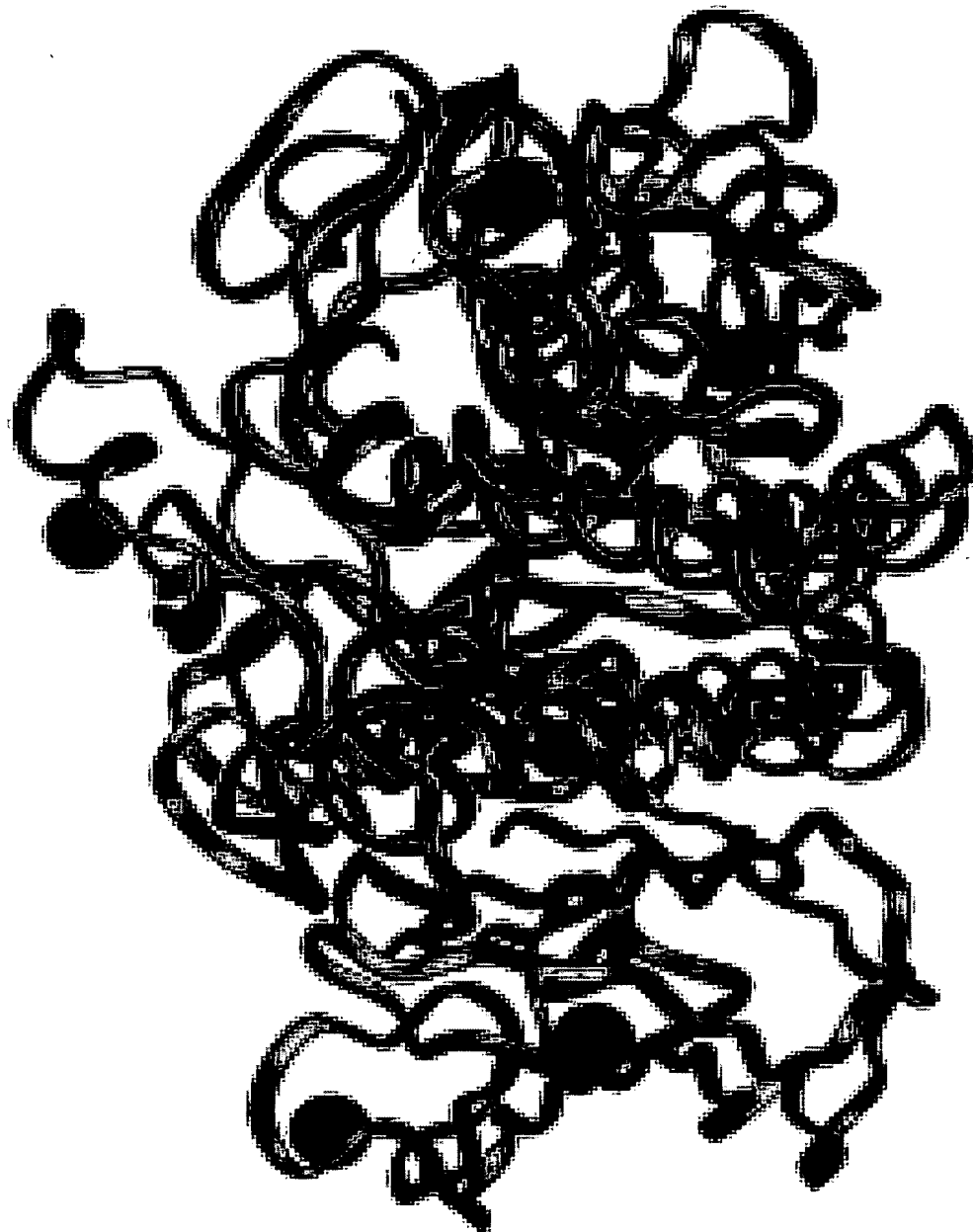


Fig. 2

Fig. 3

[illegible]

1)	AVPS-TQTPW	GIKSIYNDQS	ITK-TTGGSG	IKVAVLDTGV	YT-----SH	LDLAGSAEQC
2)	----AQSVPY	GVSQIKAPAL	HSQ-GYTGSN	VKVAVIDSGI	DS-----SH	PDLK--VAGG
3)	----AQSVPW	GISRVQAPAA	HNR-GLTGSG	VKVAVLDTGI	S-----TH	PDL--NIRGG
4)	-----NDV	ARGIVKADVA	QNNFGLYGQG	QIVAVADTGL	DTGRNDSSMH	EAFRGKITAL
	1					53
1)	KDFTQSNPLV	DGSC-TDRQG	HGTHVAGTVL	AHGGSNQGQV	YGVAPQAKLW	AYKVLGD-NG
2)	ASMVPSET--	--PNFQDDNS	HGTHVAGTVA	ALN--NSIGV	LGVAPSSALY	AVKVLGD AG
3)	ASFVPGEF--	--ST-QDGNG	HGTHVAGTIA	ALN--NSIGV	LGVAPSAELY	AVKVLGA-SG
4)	YALG-RTN--	--NA-NDPNG	HGTHVAGSVL	GN---ATNKG	MAPQANLVFQ	SIMD-SGGGL
	54					106
1)	SGY--SDD-I	AAAIRHVADE	ASRTGSKVVI	NMSLGSSA--	-KDSLIASAV	DYAY-GKGV
2)	SGQ--YSW-I	INGIEWAIA	N-----MDVI	NMSLGGPS--	-GSAALKA	DKAV-ASGV
3)	SGS--VSS-I	AQGLEWAGN	G-----MHVA	NLSLGSPS--	-PSATLEQ	NSAT-SRGV
4)	GGLPA-NLQT	LFSQAYSAGA	R-----IHTN	SWGAPVNGAY	TTDSRN-VDD	YVRKNDMTIL
	107					156
1)	IVAAAGNSGS	G---SNTIGF	PGGLVNAVAV	AALN-----	-----VQQNG	TYRVADFSSR
2)	VVAAAGNEG-	STGSSSTVGY	PGKYPSVIAV	GAVDS-----	-----S----	-NQRASFSSV
3)	VVAASGNSGA	-----GSISY	PARYANAMAV	GATDQ-----	-----N----	-NNRASFSQY
4)	FAAGNEGPGS	G---TISAPG	TAKNAITVGA	TENLRPSFGS	YADNIN----	-HVAQFSSRG
	157					208
1)	GNPATAGDYI	IQERDIEVSA	PGASVESTWY	T-----	---GGYNTIS	GTSMATPHVA
2)	GP-----	----ELDVMA	PGVSIQSTLP	G-----	---NKYGAYN	GTSMASPHVA
3)	GA-----	----GLDIVA	PGVNVQSTYP	G-----	---STYASLN	GTSMATPHVA
4)	PTRDGRIK--	----PDVMAP	GTIILSARSS	LAPDSSFWAN	HDSKYAYMGG	TSMATPIVAG
	209					262
1)	GLAAKIWSAN	T-----SLSH	SQLRTELQNR	AKVYDIKGGI	GAGTGDDYAS	GFGYPRVK--
2)	GAAALILSKH	P-----NWTN	TQVRSSLQNT	T--TKLG---	-----DSFYY	GKGLINVQAA
3)	GAAALVKQKN	P-----SWSN	VQIRNHLKNT	A--TSLG---	-----STNLY	GSGLVNAEAA
4)	NVAQLREHFV	KNRGVTPKPS	LLKAALIAGA	A--DVGLGFP	-----NGNQG	WGRVTLDKSL
	263					315
1)	-----	-----	-----	-----	-----	-----
2)	AQ-----	-----	-----	-----	-----	-----
3)	TR-----	-----	-----	-----	-----	-----
4)	NVAFVNETSP	LSTSQKATYS	FTAQAGKPLK	ISLVWSDAPG	STTASLTLVN	DLDLVITAPN
	316					375
1)	-----	-----	-----	-----	-----	-----
2)	-----	-----	-----	-----	-----	-----
3)	-----	-----	-----	-----	-----	-----
4)	GTKYVGNDFT	APYDNNWDGR	NNVENVFINA	PQSGTYTVEV	QAYNVPVGPQ	TFSLAIVH
	376					433

Fig. 4